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<110> Mahajan, Pramod B.  
<120> Mre11 Orthologue and Uses Thereof  
  
<130> 1264D  
  
<150> US 09/835,654  
<151> 2001-04-16  
  
<150> US 60/198,570  
<151> 2000-04-19  
  
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<170> FastSEQ for Windows Version 3.0  
  
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<212> DNA  
<213> Zea mays  
  
<220>  
<221> CDS  
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1

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| cta ttc cat gag aac aag ccg tca cgc tca acc ctg gta aaa acg att | 462 |
| Leu Phe His Glu Asn Lys Pro Ser Arg Ser Thr Leu Val Lys Thr Ile | |
| 90 95 100 | |
| gag att cta cgg cgc tac tgc cta aat gat caa cct gtg aag ttc cag | 510 |
| Glu Ile Leu Arg Arg Tyr Cys Leu Asn Asp Gln Pro Val Lys Phe Gln | |
| 105 110 115 120 | |
| gtt gtc agt gat cag aca gtt aac ttt cca aac agg ttt ggt aag gta | 558 |
| Val Val Ser Asp Gln Thr Val Asn Phe Pro Asn Arg Phe Gly Lys Val | |
| 125 130 135 | |
| aat tat gaa gac cca aac ttt aac gtt ggt ctg cct gtg ttc acc att | 606 |
| Asn Tyr Glu Asp Pro Asn Phe Asn Val Gly Leu Pro Val Phe Thr Ile | |
| 140 145 150 | |
| cat gga aat cat gat gac cct gct gga gtg gat aat ctc tct gct atc | 654 |
| His Gly Asn His Asp Asp Pro Ala Gly Val Asp Asn Leu Ser Ala Ile | |
| 155 160 165 | |
| gat att ctt tcg gct tgc aat ctt gta aat tat ttt gga aag atg gac | 702 |
| Asp Ile Leu Ser Ala Cys Asn Leu Val Asn Tyr Phe Gly Lys Met Asp | |
| 170 175 180 | |
| ctt ggt ggc tct ggc gtt ggt cag ata gca gtt tat cct gta ctt gta | 750 |
| Leu Gly Gly Ser Gly Val Gly Gln Ile Ala Val Tyr Pro Val Leu Val | |
| 185 190 195 200 | |
| aaa aag ggc atg act tca gtt gca ctg tat ggt ctt gga aac att aga | 798 |
| Lys Lys Gly Met Thr Ser Val Ala Leu Tyr Gly Leu Gly Asn Ile Arg | |
| 205 210 215 | |
| gat gaa cga cta aat aga atg ttt cag acg cct cat tca gta cag tgg | 846 |
| Asp Glu Arg Leu Asn Arg Met Phe Gln Thr Pro His Ser Val Gln Trp | |
| 220 225 230 | |
| atg cga cct gga act caa gat ggg gag tca gcg tct gac tgg ttc aat | 894 |
| Met Arg Pro Gly Thr Gln Asp Gly Glu Ser Ala Ser Asp Trp Phe Asn | |
| 235 240 245 | |
| ata ttg gta ctt cat cag aat agg ata aag aca aac cct aaa agt gcc | 942 |
| Ile Leu Val Leu His Gln Asn Arg Ile Lys Thr Asn Pro Lys Ser Ala | |
| 250 255 260 | |
| atc aat gag cat ttc tta cca ggt tca tca gtc gcg acg tcc ctg att | 990 |
| Ile Asn Glu His Phe Leu Pro Gly Ser Ser Val Ala Thr Ser Leu Ile | |
| 265 270 275 280 | |
| gat ggt gaa gca aaa cca aag cat gtt ctt ttg tta gaa atc aag gga | 1038 |
| Asp Gly Glu Ala Lys Pro Lys His Val Leu Leu Glu Ile Lys Gly | |
| 285 290 295 | |
| aat cag tac agg cca acc aaa ata cct ctg aga tct gtc aga cct ttt | 1086 |
| Asn Gln Tyr Arg Pro Thr Lys Ile Pro Leu Arg Ser Val Arg Pro Phe | |
| 300 305 310 | |

| | |
|---|------|
| gaa tat gct gag gtt gtg ttg aaa gat gaa gca gat gtt aac tca aat Glu Tyr Ala Glu Val Val Leu Lys Asp Glu Ala Asp Val Asn Ser Asn 315 320 325 | 1134 |
| gat cag gac tct gtg ctt gaa cat ttg gat aaa att gta aga aat ctg Asp Gln Asp Ser Val Leu Glu His Leu Asp Lys Ile Val Arg Asn Leu 330 335 340 | 1182 |
| att gag aag agt agc caa cca act gcc agc aga tca gag ccc aaa ctt Ile Glu Lys Ser Ser Gln Pro Thr Ala Ser Arg Ser Glu Pro Lys Leu 345 350 355 360 | 1230 |
| cca tta gtt aga atc aag gta gat tac tct ggg ttt tca aca ata aac Pro Leu Val Arg Ile Lys Val Asp Tyr Ser Gly Phe Ser Thr Ile Asn 365 370 375 | 1278 |
| cca caa cgt ttt ggt cag aag tat gtt gga aag gtc gca aac cct caa Pro Gln Arg Phe Gly Gln Lys Tyr Val Gly Lys Val Ala Asn Pro Gln 380 385 390 | 1326 |
| gat att ctc att ttc tca aaa tca gca aag aag cgc cag act aca gga Asp Ile Leu Ile Phe Ser Lys Ser Ala Lys Lys Arg Gln Thr Thr Gly 395 400 405 | 1374 |
| gat cac att gat gat tct gag aaa ctt cgt cct gag gaa cta aac caa Asp His Ile Asp Asp Ser Glu Lys Leu Arg Pro Glu Glu Leu Asn Gln 410 415 420 | 1422 |
| caa aca atc gaa gct ctg gtc gca gag agt aac ttg aaa atg gag att Gln Thr Ile Glu Ala Leu Val Ala Glu Ser Asn Leu Lys Met Glu Ile 425 430 435 440 | 1470 |
| ctt ccg gtt gat gat ttg gac att gcg ttg cat gat ttt gtg aac aag Leu Pro Val Asp Asp Leu Asp Ile Ala Leu His Asp Phe Val Asn Lys 445 450 455 | 1518 |
| gat gac aag atg gca ttt tat tca tgt ttg cag aga aac ctt gaa gaa Asp Asp Lys Met Ala Phe Tyr Ser Cys Leu Gln Arg Asn Leu Glu Glu 460 465 470 | 1566 |
| acc agg aat aag ttg agt tct gaa gca gat aaa tcc aaa ttt gag gaa Thr Arg Asn Lys Leu Ser Ser Glu Ala Asp Lys Ser Lys Phe Glu Glu 475 480 485 | 1614 |
| gaa gat ata ata gtc aaa gtt ggc gag tgc atg cag gaa cgc gtt aag Glu Asp Ile Ile Val Lys Val Gly Glu Cys Met Gln Glu Arg Val Lys 490 495 500 | 1662 |
| gaa agg tct ctg cac tct aag gac ggc aca cgt ttg aca aca ggc tct Glu Arg Ser Leu His Ser Lys Asp Gly Thr Arg Leu Thr Thr Gly Ser 505 510 515 520 | 1710 |
| cac aac ttg gtg ttt aat tat ctg agc ctt aat atc ttt tct ttt tgt His Asn Leu Val Phe Asn Tyr Leu Ser Leu Asn Ile Phe Ser Phe Cys | 1758 |

| | | | |
|---------------------------------|---------------------------------|-----|------|
| 525 | 530 | 535 | |
| att ttt cct ggg gct gga tac tgg | aca gct agt aac tct tac aac ctt | | 1806 |
| Ile Phe Pro Gly Ala Gly Tyr Trp | Thr Ala Ser Asn Ser Tyr Asn Leu | | |
| 540 | 545 | 550 | |

| | | | | | | |
|------------|-------------|-------------|-------------|------------|------------|------|
| taactaggat | actggaggta | aatctttttac | agctcaaagc | aaccagaact | ccttcagtga | 1866 |
| tgatgaagac | accagggaga | tgctttcttgg | tgcaagatca | actgatgttg | gacgaaaatc | 1926 |
| atctggattt | actagaccct | ccaaagatac | tgctgatgtt | gctaaacgtg | gtacttccaa | 1986 |
| aagaggcagg | ggaagaggca | ccagttcaat | gaagcagacc | actcttagtt | tcagccagtc | 2046 |
| aaggtcagct | accgttattc | gtagtgagga | tgtggcttcc | tctgaggagg | aagcagatgc | 2106 |
| aaatgaagtt | gttgaaaatt | cagaagagga | gagtgcgcaa | caagttggac | gtaaaagagc | 2166 |
| agctcctagg | ggtagaggta | gaggtagagg | cggagggttcc | actgcaaaga | gggggcgaaa | 2226 |
| aacagatatt | gcttccatgc | aaaatatgat | gagcaaagat | gatgatgatt | cagaagatga | 2286 |
| accgccaaag | aaaactcctc | gggtcaccag | gaactatggc | gctgtcagga | ggagatgacc | 2346 |
| ctttaaggag | ttcttgctca | tgagagttat | aggctaggtg | ttttgtcttg | taaagttgga | 2406 |
| agagccgacg | tgTTTTtattc | aaccttgacg | tcgaccagtt | tgcggtgccc | tgaactgact | 2466 |
| gtaccttgta | cacgccccgaa | tgtaacggat | ttttgggatt | tatacatcct | tgtagctgct | 2526 |
| taaattccag | cgattgctgt | caaatgaact | tcgggaaaaa | aaaaaaaaaa | aaaaaaaaaa | 2586 |
| aaaaaaaaaa | a | | | | | 2597 |

<210> 2
 <211> 552
 <212> PRT
 <213> Zea mays

<400> 2

| | |
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| Met Val Gly Phe Cys Ser Ala Leu Asp Leu Gln Gln Arg Ile Gly Leu | |
| 1 5 10 15 | |
| Ala Asn Thr Leu Ser Ser Gly Ser Met Ser Glu Pro Ala Gln Pro Ser | |
| 20 25 30 | |
| Gly Gly Glu Gly Asp Val Asn Thr Leu Arg Ile Leu Val Ala Thr Asp | |
| 35 40 45 | |
| Cys His Leu Gly Tyr Met Glu Lys Asp Glu Ile Arg Arg Phe Asp Ser | |
| 50 55 60 | |
| Phe Gln Ala Phe Glu Glu Ile Cys Ala Leu Ala Asp Lys Asn Lys Val | |
| 65 70 75 80 | |
| Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser | |
| 85 90 95 | |
| Arg Ser Thr Leu Val Lys Thr Ile Glu Ile Leu Arg Arg Tyr Cys Leu | |
| 100 105 110 | |
| Asn Asp Gln Pro Val Lys Phe Gln Val Val Ser Asp Gln Thr Val Asn | |
| 115 120 125 | |
| Phe Pro Asn Arg Phe Gly Lys Val Asn Tyr Glu Asp Pro Asn Phe Asn | |
| 130 135 140 | |
| Val Gly Leu Pro Val Phe Thr Ile His Gly Asn His Asp Asp Pro Ala | |
| 145 150 155 160 | |
| Gly Val Asp Asn Leu Ser Ala Ile Asp Ile Leu Ser Ala Cys Asn Leu | |
| 165 170 175 | |
| Val Asn Tyr Phe Gly Lys Met Asp Leu Gly Gly Ser Gly Val Gly Gln | |
| 180 185 190 | |
| Ile Ala Val Tyr Pro Val Leu Val Lys Lys Gly Met Thr Ser Val Ala | |
| 195 200 205 | |
| Leu Tyr Gly Leu Gly Asn Ile Arg Asp Glu Arg Leu Asn Arg Met Phe | |
| 210 215 220 | |
| Gln Thr Pro His Ser Val Gln Trp Met Arg Pro Gly Thr Gln Asp Gly | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Glu | Ser | Ala | Ser | Asp | Trp | Phe | Asn | Ile | Leu | Val | Leu | His | Gln | Asn | Arg |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Lys | Thr | Asn | Pro | Lys | Ser | Ala | Ile | Asn | Glu | His | Phe | Leu | Pro | Gly |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Ser | Val | Ala | Thr | Ser | Leu | Ile | Asp | Gly | Glu | Ala | Lys | Pro | Lys | His |
| | | 275 | | | | 280 | | | | | | 285 | | | |
| Val | Leu | Leu | Leu | Glu | Ile | Lys | Gly | Asn | Gln | Tyr | Arg | Pro | Thr | Lys | Ile |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Pro | Leu | Arg | Ser | Val | Arg | Pro | Phe | Glu | Tyr | Ala | Glu | Val | Val | Leu | Lys |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Asp | Glu | Ala | Asp | Val | Asn | Ser | Asn | Asp | Gln | Asp | Ser | Val | Leu | Glu | His |
| | | | 325 | | | | | 330 | | | | | | 335 | |
| Leu | Asp | Lys | Ile | Val | Arg | Asn | Leu | Ile | Glu | Lys | Ser | Ser | Gln | Pro | Thr |
| | | | 340 | | | | 345 | | | | | | 350 | | |
| Ala | Ser | Arg | Ser | Glu | Pro | Lys | Leu | Pro | Leu | Val | Arg | Ile | Lys | Val | Asp |
| | 355 | | | | | 360 | | | | | | 365 | | | |
| Tyr | Ser | Gly | Phe | Ser | Thr | Ile | Asn | Pro | Gln | Arg | Phe | Gly | Gln | Lys | Tyr |
| 370 | | | | | 375 | | | | | | 380 | | | | |
| Val | Gly | Lys | Val | Ala | Asn | Pro | Gln | Asp | Ile | Leu | Ile | Phe | Ser | Lys | Ser |
| 385 | | | | | 390 | | | | 395 | | | | | | 400 |
| Ala | Lys | Lys | Arg | Gln | Thr | Thr | Gly | Asp | His | Ile | Asp | Asp | Ser | Glu | Lys |
| | | | 405 | | | | | 410 | | | | | | 415 | |
| Leu | Arg | Pro | Glu | Glu | Leu | Asn | Gln | Gln | Thr | Ile | Glu | Ala | Leu | Val | Ala |
| | | 420 | | | | | 425 | | | | | | 430 | | |
| Glu | Ser | Asn | Leu | Lys | Met | Glu | Ile | Leu | Pro | Val | Asp | Asp | Leu | Asp | Ile |
| | 435 | | | | | 440 | | | | | 445 | | | | |
| Ala | Leu | His | Asp | Phe | Val | Asn | Lys | Asp | Asp | Lys | Met | Ala | Phe | Tyr | Ser |
| 450 | | | | | 455 | | | | | 460 | | | | | |
| Cys | Leu | Gln | Arg | Asn | Leu | Glu | Glu | Thr | Arg | Asn | Lys | Leu | Ser | Ser | Glu |
| 465 | | | | 470 | | | | | 475 | | | | | | 480 |
| Ala | Asp | Lys | Ser | Lys | Phe | Glu | Glu | Glu | Asp | Ile | Ile | Val | Lys | Val | Gly |
| | | | 485 | | | | | 490 | | | | | | 495 | |
| Glu | Cys | Met | Gln | Glu | Arg | Val | Lys | Glu | Arg | Ser | Leu | His | Ser | Lys | Asp |
| | | 500 | | | | | 505 | | | | | | 510 | | |
| Gly | Thr | Arg | Leu | Thr | Thr | Gly | Ser | His | Asn | Leu | Val | Phe | Asn | Tyr | Leu |
| | 515 | | | | | 520 | | | | | | 525 | | | |
| Ser | Leu | Asn | Ile | Phe | Ser | Phe | Cys | Ile | Phe | Pro | Gly | Ala | Gly | Tyr | Trp |
| 530 | | | | | 535 | | | | | 540 | | | | | |
| Thr | Ala | Ser | Asn | Ser | Tyr | Asn | Leu | | | | | | | | |
| 545 | | | | | 550 | | | | | | | | | | |

<210> 3
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 3
 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa

<210> 4
 <211> 2308
 <212> DNA
 <213> Zea mays

<400> 4

| | | | | | | |
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| ccgactgcca | tctaggctac | atggagaaaag | atgagatacg | taggtttgat | tcctttcaag | 60 |
| catttgagga | gatttgcgca | ttggcagata | aaaataaggt | ggattttata | cttctcgggtg | 120 |
| gtgatctatt | ccatgagaac | aagccgtcac | gctcaaccct | ggtaaaaaacg | attgagattc | 180 |
| tacggcgcta | ctgcctaaat | gatcaacctg | tgaagttcca | ggttgtcagt | gatcagacag | 240 |
| ttaaactttcc | aaacagggtt | ggtaaggtaa | attatgaaga | cccaaacttt | aacgttgggtc | 300 |
| tgcctgtgtt | caccattcat | ggaaatcatg | atgaccctgc | tggagtggat | aatctctctg | 360 |
| ctatcgatat | tctttcggct | tgcaatcttg | taaattat | tggaaagatg | gaccttgggtg | 420 |
| gctctggcgt | tggtcagata | gcagtttata | ctgtacttgt | aaaaaagggc | atgacttcag | 480 |
| ttgcactgta | tggctcttga | aacattagag | atgaacgact | aaatagaatg | tttcagacgc | 540 |
| ctcattcagt | acagtggatg | cgacctggaa | ctcaagatgg | ggagtcagcg | tctgactggt | 600 |
| tcaatatatt | ggtacttcat | cagaatagga | taaagacaaa | ccctaaaagt | gccatcaatg | 660 |
| agcatttctt | accaggttca | tcagtcgcga | cgtccctgat | tgatggtgaa | gcaaaaccaa | 720 |
| agcatgttct | tttggttagaa | atcaagggaa | atcagtacag | gccaacccaa | atacctctga | 780 |
| gatctgtcag | accttttgaa | tatgctgagg | ttgtgttgaa | agatgaagca | gatgttaact | 840 |
| caaatgatca | ggactctgtg | cttgaacatt | tgataaaaat | tgtgaagaaat | ctgattgaga | 900 |
| agagtagcca | accaactgcc | agcagatcag | agcccaaact | tccattagtt | agaatcaagg | 960 |
| tagattactc | tgggttttca | acaataaacc | cacaacgttt | tggtcagaag | tatgttgtaa | 1020 |
| aggctcgaaa | ccctcaagat | attctcattt | tctcaaaatc | agcaaagaag | cgccagacta | 1080 |
| caggagatca | cattgatgat | tctgagaaac | ttcgtcctga | ggaactaaac | caacaaacaa | 1140 |
| tcgaagctct | ggtcgcagag | agtaacttga | aaatggagat | tcttcggtt | gatgatttgg | 1200 |
| acattgcgtt | gcatgatttt | gtgaacaagg | atgacaagat | ggcattttat | tcatgtttgc | 1260 |
| agagaaacct | tgaagaaacc | aggaataagt | tgagttctga | agcagataaa | tccaaatttg | 1320 |
| aggaagaaga | tataatagtc | aaagttagcg | agtgcattgc | ggaacgcgtt | aaggaaagg | 1380 |
| ctctgcactc | taaggacggc | acacgtttga | caacaggctc | tcacaacttg | gtgtttaatt | 1440 |
| atctgagcct | taatatcttt | tctttttgta | tttttcctgg | ggctggatac | tggacagcta | 1500 |
| gtaactctta | caaccttta | ctaggatact | ggaggtaaat | cttttacagc | tcaaagcaac | 1560 |
| cagaactcct | tcagtgatga | tgaagacacc | aggagatgc | ttcttggtgc | aagatcaact | 1620 |
| gatgttggac | gaaaatcatc | tggatttact | agaccctcca | aagatactgc | tgatgttgct | 1680 |
| aaacgtggta | cttccaaaag | aggcagggga | agaggcacca | gttcaatgaa | gcagaccact | 1740 |
| cttagtttca | gccagtcaag | gtcagctacc | gttattcgta | gtgaggatgt | ggcttcctct | 1800 |
| gaggaggaag | cagatgcaaa | tgaagttggt | gaaaattcag | aagaggagag | tgcgcaacaa | 1860 |
| gttgagcgtg | aaagagcagc | tcctaggggt | agaggtagag | gtagaggcgg | aggttccact | 1920 |
| gcaaagaggg | ggcgaaaaac | agatattgct | tcctatgcaa | atatgatgag | caaagatgat | 1980 |
| gatgattcag | aagatgaacc | gccaaagaaa | actcctcggt | tcaccaggaa | ctatggcgct | 2040 |
| gtcaggagga | gatgaccctt | taaggagttc | ttgctcatga | gagttatagg | ctaggtgttt | 2100 |
| tgtcttgtaa | agttggaaga | gccgacgtgt | ttttatcaac | cttgacgtcg | accagtttgc | 2160 |
| gttgccgtga | actgactgta | ccttgtaac | gccgaatgt | aacggatttt | tgggatttat | 2220 |
| acatccttgt | agctgcttaa | attccagcga | ttgctgtcaa | atgaacttcg | ggaaaaaaa | 2280 |
| aaaaaaaaa | aaaaaaaaa | aaaaaaaaa | | | | 2308 |

<210> 5
 <211> 396
 <212> DNA
 <213> Zea mays

<400> 5

| | | | | | | |
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| tcgaccacg | cgtccggccg | gcccttctct | tcccttgctg | ctgtgcgaac | ccgagcgccc | 60 |
| aaacctgaac | ttaaagctatt | tggggctact | tgtatttgga | aaaaatatat | cgggtccttt | 120 |
| actggtccgc | cgggtgttatt | ttaacttatg | aaatggttgg | tttttgagct | gcattagatt | 180 |

| | |
|--|-----|
| tacagcaacg gattggtttg gccaacacgt tgagttcagg ttcaatgtct gaaccagcac | 240 |
| aacctagtgg aggggaaggt gatgtcaaca cgctcctaatt acttgtagca accgactgcc | 300 |
| atctaggcta catggagaaa gatgagatac gtaggtttga ttcctttcaa gcatttgagg | 360 |
| agatttgcgc attggcagat aaaaataagg tggatt | 396 |

<210> 6
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> M13R synthetic primer

| | |
|---|----|
| <400> 6 | |
| agcggataac aatttcacac aggaaacagc tatgac | 36 |

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> R1 synthetic primer

| | |
|------------------------|----|
| <400> 7 | |
| cttatttttta tctgccaatg | 20 |

<210> 8
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7 synthetic primer

| | |
|-----------------------------|----|
| <400> 8 | |
| taatacgact cactataggc cgaat | 25 |

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> R2 synthetic primer

| | |
|-----------------------|----|
| <400> 9 | |
| gcgtgacggc ttgttctcat | 20 |